

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 07-24-02
Searcher: Beverly C 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site
 STIC
 CM-1
 Pre-S

Type of Search
 N.A. Sequence
 A.A. Sequence
 Structure
 Bibliographic

Vendors
 IG
 STN
 Dialog
 APS
 Geninfo
 SDC
 DARC/Questel
 Other CGN

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 13:10:30 ; Search time 2538.62 Seconds
(without alignments)

Sequence: 1 tagcaggatataatagatgaa.....gggtatattgctcacaatag 309

Scoring table: IDENTITY_NUC Gapov 10.0 , Gapext 1.0

Searched: US-09-738-599-22

Perfect score: 1642.845 Million cell updates/sec

Minimum DB seq. length: 0

Maximum DB seq. length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_estnum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpi:*

7: em_estro:*

8: em_htc:*

9: qb_esti:*

10: qb_est2:*

11: qb_htc:*

12: qb_gss:*

13: em_gss_hum:*

14: em_gss_inv:*

15: em_gss_pn:*

16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8 SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	228.6	74.0	332	9 AW619529
C 2	183.9	59.5	731	9 AV398499
C 3	140.4	45.4	240	9 AW595631
C 4	139.8	45.2	785	9 A1567008
C 5	123.8	40.1	223	10 C22108
C 6	117.2	37.9	160	10 BG95793
C 7	115.6	37.4	160	10 BG95172
C 8	109.3	35.4	336	10 BE251841
C 9	106.2	34.4	162	10 BE338974
C 10	88.4	28.6	178	10 BI432815
C 11	65.8	21.3	802	9 A146999
C 12	59.8	19.4	594	10 BE93915
C 13	45.2	14.6	560	12 B84811
C 14	45.2	14.6	634	12 A030897
C 15	42.8	13.9	532	12 A0244521
C 16	42.6	13.6	299	9 A0547917
C 17	38.8	12.6	914	12 A2539756

18 ALIGNMENTS

RESULT	1
AW619529/c	AW619529
LOCUS	AW619529
DEFINITION	PBE Sus scrofa cDNA 5', mRNA sequence.
ACCESSION	AW619529
VERSION	AW619529.1
KEYWORDS	EST
SOURCE	Sus scrofa
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suis; Suidae; Sus.
REFERENCE	1 (bases 1 to 332)
AUTHORS	Smith, T.P.L., Fahrnerkug, S.C., Rohrer, G.A., Simmen, F.A., Rexroad, C.E. and Keele, J.W.
TITLE	Mapping of expressed sequence tags from a porcine early embryonic cDNA library. Anim. Genet. 32 (2), 66-72 (2001)
JOURNAL	Anim. Genet.
MEDLINE	21314990
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center, PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov

19 FEATURES

FORWARD: GGAAACAGCTATGGCCATG
BACKWARD: GTTAAACACCGGGCAGT
Seq primer: ATTAAACCCCTACTAAAGGG.
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Location/Qualifiers
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<lab_host="X10LR"
<note="Vector: PBLUESCRIPT SK-; Site_1: EcoRI; Site_2:
XhoI; Library made from pool of embryos in spherical and

filamentous stages of development (7.5% and 92.5%, respectively of each stage) as described in *Shoemaker* et al.

BASE COUNT
ORIGIN 94 a 68 c 139, 145, 96 t 1990.

Query Match 74.0%; Score 228.6; DB 9; Length 332;
 Best Local Similarity 92.7%; Pred. NO. 2.1e-52;
 Matches 240; Conservative 0; Mismatches 19; Indels 0; Gaps 0

Qy	50	tgcttattacagatgtgtctcaacaaacgtttactgtgtggaaacaaacggacagcagtaa	109
Db	332	TGCTTATTACAGATGTGTCTCAACAAACGGACAGCAGTAACAAACGGACAGTC	273

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Qy	230	catcgtaaaaggatgtctcggttttactttggactactcgactcgatggacc	289
Db	152	CATTCGIAAATGATGATGCTCGGTTAATCTTACTTTAGGAAATATRACTCCGCTGGAGCC	93

DBS1173M 92 GNGTGTATTCGTCACAATA 74

RESULT 2
AV398499
LOCUS AV398499
DEFINITION Bombyx mori ovary BmNPV infected: 2 hr after inoculation
VERSION 1
ACCESSION AV398499
KEYWORDS linear EST 05-FEB-2000
MATERIALS mRNA
METHODS linear EST 05-FEB-2000
SEQUENCE BmNPV
SOURCE BmNPV
SPECIES Bombyx mori
STRAIN BmNPV
TAXONOMY Bombyx mori
VERSION 1
KEYWORDS mRNA
METHODS linear EST 05-FEB-2000
SEQUENCE BmNPV
SOURCE BmNPV
SPECIES Bombyx mori
STRAIN BmNPV
TAXONOMY Bombyx mori

DEFINITION Av338499 Bombyx mori ovar BmNPV infected; 2 hr after inoculation Bombyx mori CLONE NV0211882 T3, mRNA sequence.

KEYWORD
EST.
domestic silkworm.
SOURCE
ORGANISM
Bombyx mori

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.

AUTHORS Mita, R., Morimoto, M., Shimada, T., Okano, K. and Maeda, S.
TITLE Bombyx mori cDNA
JOURNAL Unpublished (2000)

COMMENT
Contract: Mita K
Genome Research Group
National Institute of Radiological Sciences

method: kmtaenrs.go.jp
 method:uni-directional, sequence direction:sequenced from T3 prime
 (5' -> 3')
 Project-'Silkworm Genome Program in MAFF', and Research for the
 Future Program in JSSP'. see 'SilkBase',
<http://www.ab.a.u-tokyo.ac.jp/silbase/>, for whole ESTdb.

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  a 194
  a 171 c 164 g 202 t

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BASE COUNT	194	a	1/1	8	104	g	202	t
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Query Match	59.5%	Score 183.8;	DB 9;	Length 731;
Best Local Similarity	91.9%	Pred. No. 47e-40;	0;	Mismatches 17;
Matches	194;	Conservative	0;	Indels 0;
DEFINITION	9104 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.	EST	25 APR-2001	
REFERENCE	AW659631			
AUTHORS	AW659631.1 GI:7425458			
VERSION				
KEYWORDS	EST.			
SOURCE	COW.			
ORGANISM	Bos taurus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bos.				
1 (bases 1 to 240)				
Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.B., White, J., Cho, J., Fahrekrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Cliftko-Mckown, C.G., Perrea, G., Holt, I., Karayicheva, S., Liang, F., Quackenbush, J. and Keele, J.W.				
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle			
JOURNAL	Genome Res. 11 (4), 626-630 (2001)			
MEDLINE	21180013			
COMMENT	Contact: Smith TPL USA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4390 Fax: 402 762 4390			
Email: smith@marc.usda.gov				
FORWARD:	AGGAACAGCTATGACCAT			
BACKWARD:	GTTCGCCGTCAGGACG			
Plate: 66	Row: N	Column: 3		
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	Library made from pooled tissue from lymph node, ovary, fat, hypophalamus, and pituitary."			
ORIGIN				
BASE COUNT	70 a 51 c 52 g 67 t			
Quary Match	45.4%	Score 140.4;	DB 9;	Length 240;
Best Local Similarity	90.4%	Pred. No. 3.2e-28;		

Matches	150;	Conservative	0;	Mismatches	16;	Indels	0;	Gaps	0;
QY	143	tttcggaaatggacaaggaaacttcggaaatgttcgtatgcggccaaatgtgggggtcagaaa	202						
Db	240	TTCTGGAAATGGCAGAGAAACTGTGCCATGCCAATTTGGGGCCAGAA	181						
QY	203	atgtgtttaaacggaaacttcggaaatgttcgtatgcggccaaatgtgggggtcagaaa	202						
Db	180	ATGTTGTTAACAGAACCCACCAACATTCGAAATGGATCTCGGTTTAACTT	121						
QY	263	ttgcacatataccctcggtggaaacccggatattgtccacaata	308						
Db	120	TAGCATTATACTCCCCCTGGAAGCGCGTGTGATGCTCCAA	75						
RESULT	4								
LOCUS	AT547008	785 bp	mRNA	linear	EST	09-AUG-1999			
DEFINITION	PM2.1.13_C01.r mynorm	Homo sapiens	cdNA 5'	mRNA sequence.					
ACCESSION	AT547008								
VERSION	AT547008.1								
KEYWORDS									
SOURCE									
ORGANISM	Homo sapiens								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. I (bases 1 to 785)									
AUTHORS	Ruang, G.M., Ng, W.I., Farkas, J., He, L., Liang, H.A., Gordon, D., Yu, J. and Hood, L.								
TITLE	Prostate cancer expression profiling by cdna sequencing analysis								
JOURNAL	Genomics 59 (2), 178-186 (1999)								
MEDLINE	99339982								
COMMENT	University of Washington Contact: Guyang Matthew Huang Leroy Hood								
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1.	785	/organism="Homo sapiens"							
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SOURCE	Pig	JOURNAL	Unpublished (2000)	
ORGANISM	Sus scrofa	COMMENT	Contact: Smith TPL	
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	USDA, ARS, US Meat Animal Research Center	PO Box 155, Clay Center, NE 68933-0166, USA		
Mammalia; Eutheria; Cetartiodactyla; Sina; Suidae; Sus.	Tel: 402 762 4366	Fax: 402 762 4390		
REFERENCE	1 (bases 1 to 160)	Email: smithe@email.usda.gov		
AUTHORS	Fahrhenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Gross, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.	Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.		
TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine	PCR PRIMERS	PCR Primers	
VERSION	Unpublished (2000)	FORWARD: AGGAACAGCTATGACCAT	FORWARD: AGGAACAGCTATGACCAT	
KEYWORDS	Contact: Smith TPL	BACKWARD: GTTTCAGTCAGGACG	BACKWARD: GTTTCAGTCAGGACG	
EST	USDA, ARS, US Meat Animal Research Center	Plate: 116	Plate: 116	
ORGANISM	PO Box 155, Clay Center, NE 68933-0166, USA	row: L	row: L	
REFERENCE	Tel: 402 762 4366	column: 23	column: 23	
AUTHORS	Fax: 402 762 4390	Seq primer: ATTAGCTGACATATAG.	Seq primer: ATTAGCTGACATATAG.	
COMMENT	Email: smithe@email.usda.gov	Location/Qualifiers	Location/Qualifiers	
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	/clone_lib="MARC 1PIG"	/clone_lib="MARC 1PIG"	/clone_lib="MARC 1PIG"	
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	Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos	/notes="Vector: PCMV SPOR6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos"	/notes="Vector: PCMV SPOR6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos"	
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.8%	Score	117.2; DB 10; Length 160;	
Matches	122;	Pred.	No. 7.1e-22;	
Conservative	0;	Mismatches	8;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
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Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
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	Indels	0;	Gaps	0;
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Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
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	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g 45 t	
ORIGIN		ORIGIN		
Query Match	37.9%	Query Match	37.4%	
Best Local Similarity	93.1%	Score	115.6; DB 10; Length 160;	
Matches	121;	Pred.	No. 1.9e-21;	
Conservative	0;	Mismatches	9;	
	Indels	0;	Gaps	0;
BASE COUNT	46 a 37 c 31 g 46 t	BASE COUNT	47 a 37 c 31 g	

BASE COUNT	46 a	34 c	40 g	58 t
ORIGIN	BB493915	BB433915	594 bp	mRNA
DEFINITION	WHE1276_B06_C1225 Secale cereale anther cDNA library Secale cereale	DEFINITION	WHE1276_B06_C1225 Secale cereale anther cDNA library Secale cereale	
ACCESSION	BE433915	BE433915	LINEAR	EST 02-AUG-2000
VERSION	BE433915.1	GT: 96605058	EST	
KEYWORDS	rye; Secale cereale; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae	SOURCE	rye; Secale cereale	
REFERENCE	1. Triticeae; Secale; 1. (bases 1 to 594); Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, G.C., Kang, J., Lazio, G.R., Miller, R., Raasch, C.J., Ross, R., Seaton, C.L. and Tong, J.C.	ORGANISM	Secale cereale	
AUTHORS	1. Huang, G.M., Ng, W.L., Farkas, J., He, L., Liang, H.A., Gordon, D., Yu, J. and Hood, L.	COMMENT	The structure and function of the expressed portion of the wheat genomes - Antirrhinum cDNA library from rye	
TITLE	Prostate cancer expression profiling by cDNA sequencing analysis	VERSION	Unpublished (2000)	
JOURNAL	Genomics 59 (2), 178-186 (1999)	KEYWORDS	Contract: Olin Anderson	
MEDLINE	99339982	SOURCE	US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center	
REFERENCE	1. (bases 1 to 802); Huang, G.M., Ng, W.L., Farkas, J., He, L., Liang, H.A., Gordon, D., Yu, J. and Hood, L.	COMMENT	800 Buchanan Street, Albany, CA 94710, USA	
AUTHORS	1. Leroy Hood	VERSION	Tel: 5105957733 Fax: 5105958118	
TITLE	University of Washington	KEYWORDS	Email: oandern@pw.usda.gov	
JOURNAL	Department of Molecular Biotechnology, Box 357730, University of Washington, Seattle, WA 98195	SOURCE	Sequence have been trimmed to remove vector sequence and low quality sequence with printed score less than 20	
MEDLINE	Tel: 5105280100 Fax: 5105280108 Email: huangg@yahoo.com	FEATURES	Seq primer: Stratagene SK primer. Location/qualifiers	
COMMENT	Contact: Guyang Matthew Huang	COMMENT	1. .994	
FEATURES	source	1. .994	/organism="Secale cereale" 'cultivar="Blanco'"	
SOURCES	Location/Qualifiers	1. .994	/db_xref="taxon:4550"	
FEATURES	source	1. .994	/clone="WHE1276_B06_C12"	
FEATURES	source	1. .994	/clone_id="Secale cereale anther cDNA library"	
FEATURES	source	1. .994	/tissue_type="Anther"	
FEATURES	source	1. .994	/dev_stage="Adult plant before anthesis"	
FEATURES	source	1. .994	/lab_host="E. coli SOLR"	
FEATURES	source	1. .994	/note="Vector: Lambda Uni-ZAP XR, excised phagemid;"	
FEATURES	source	1. .994	Site_1: EcoRI; Site_2: XbaI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give phagemids in the TU Close Lab (Close, Fenton) at the University of California, Riverside.	
FEATURES	source	1. .994	Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."	
FEATURES	source	1. .994	BASE COUNT	
FEATURES	source	1. .994	179 a 152 c 163 g 183 t 125 others	
FEATURES	source	1. .994	ORIGIN	
FEATURES	source	1. .994	BB4811	
FEATURES	source	1. .994	LOCUS	
FEATURES	source	1. .994	BB4811	
FEATURES	source	1. .994	DEFINITION	
FEATURES	source	1. .994	RPCI-11-28F7.TP RPCI-11 Homo sapiens genomic clone RPCI-11-28F7, DNA sequence.	
FEATURES	source	1. .994	ACCESSION	
FEATURES	source	1. .994	BB4811	
FEATURES	source	1. .994	Query Match	
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FEATURES	source	1. .994	Query Match	
FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
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FEATURES	source	1. .994	Query Match	
FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
FEATURES	source	1. .994	Matches 70; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	
FEATURES	source	1. .994	Query Match	
FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
FEATURES	source	1. .994	Matches 70; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	
FEATURES	source	1. .994	Query Match	
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FEATURES	source	1. .994	Query Match	
FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
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FEATURES	source	1. .994	Query Match	
FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
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FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
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FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
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FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
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FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
FEATURES	source	1. .994	Matches 70; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	
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FEATURES	source	1. .994	Best Local Similarity 88.6%; Score 65.8; DB 9; Length 802;	
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FEATURES	source	1. .994	Matches 70; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	
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AUTHORS	I. (bases 1 to 560) Adams, M.D., Rounseley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Sun, E., Wible, C., de Jong, P. and Venter, J.C.		REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Hominoidea; Homo.
TITLE	Use of BAC End Sequences for Sequence-Ready Map Building (1998)		AUTHORS	1 (bases 1 to 644) Adams, M.D., Rounseley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Sun, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
JOURNAL	Unpublished (1998)		TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building (1998)
COMMENT	Other GSS: RPCII-28F7.TV		JOURNAL	Unpublished (1998)
CONTACT	Mark Adams		COMMENT	Other GSS: CITB1-E1-2522C3.TF
DEPARTMENT	Department of Eukaryotic Genomics		CONTACT	Shaving Zhao, William Nierman, Mark Adams
THE INSTITUTE	The Institute for Genomic Research		DEPARTMENT	Department of Eukaryotic Genomics
7912 MEDICAL CENTER DR., ROCKVILLE, MD 20850, USA			THE INSTITUTE	The Institute for Genomic Research
Tel: 301 838 0200			9712 MEDICAL CENTER DR., ROCKVILLE, MD 20850	
Fax: 301 838 0208			Tel: 301 838 0200	
EMAIL	mdadams@tigr.org		FAX	301 838 0208
CLONES	Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from Research Genetics (info@reogen.com). BAC end search page: http://www.tigr.org/tcb/hungen/bac_end_search/bac_end_search.html		EMAIL	hbe@tigr.org
PIETER@DEJONG.MED.BUFFALO.EDU			CLONES	Clones are available from Research Genetics (info@reogen.com). BAC end search page: http://www.tigr.org/tcb/hungen/bac_end_search/bac_end_search.html
BACPAC RESOURCES	(http://bacpac.med.buffalo.edu/vordering) or from Research Genetics (info@reogen.com). BAC end search page: http://www.tigr.org/tcb/hungen/bac_end_search/bac_end_search.html		SEQ PRIMER	M13 Reverse
RESEARCH GENETICS	(info@reogen.com). BAC end search page: http://www.tigr.org/tcb/hungen/bac_end_search/bac_end_search.html		CLASS	BAC ends.
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 13:45:07 ; Search time 99.46 Seconds
(without alignments)
763.128 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 309

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%, Maximum Match 100%
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCUTS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID.	Description
1	309	100.0	309	3 US-09-023-221A-22
2	309	100.0	309	4 US-09-282-352A-22
3	309	100.0	378	3 US-09-023-221A-21
4	309	100.0	378	4 US-09-282-352A-21
5	309	100.0	760	3 US-09-023-221A-1
6	309	100.0	760	4 US-09-282-352A-1
7	273	88.4	309	3 US-09-023-221A-5
8	273	88.4	309	4 US-09-282-352A-5
9	252	81.6	309	3 US-09-023-221A-6
10	252	81.6	309	4 US-09-282-352A-6
11	252	81.6	11933	4 US-09-470-618-13
12	252	81.6	11933	4 US-09-365-862-13
13	342	11.1	1519	2 US-09-0361-4
14	33.6	10.9	1817	2 US-09-743-637B-1
15	33.6	10.9	1817	3 US-08-526-840B-1
16	32.8	10.6	4380	1 07-583-945-1
17	32.8	10.6	4380	2 US-08-453-141-1
18	32.8	10.6	4380	3 US-08-293-314-1
19	32.4	10.5	1925	2 US-08-553-436A-1
20	32.2	10.4	408	4 US-09-326-111-169
21	32.2	10.4	1690	1 US-08-276-452B-24
22	32.2	10.4	1690	2 US-08-791-945-24
23	31.2	10.1	90050	4 US-09-245-041-5
24	30.6	9.9	1504	2 US-08-878-989-10
25	30.6	9.9	1504	4 US-09-272-796-10
26	30.6	9.9	1576	2 US-09-197-378-1
27	9.8	2089	1 US-08-552-142A-1	

RESULT 1

US-09-023-221A-22

Sequence 22, Appl

Patent No. 6087128

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHEILY M.

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQMENTS: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUEFFING, RAASCH & GEBHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

ZIP: 55401

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023, 221A

FILED DATE: 12-FEB-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255, 00010101

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

Query Match Best Local Similarity 100.0%; Score 309; DB 3; Length 309; Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgcaggataatagatgaa.....ggatattgtgtccacatag 60

Db 1 ATGCAGGATAATAGATGAA.....GGATATTGTGTCCACATAG 60

RESULT 12
 US-09-364-862-13
 Sequence 13, Application US/09364862
 Patent No. 6221349

GENERAL INFORMATION:
 APPLICANT: Coute, Linda B.
 APPLICANT: Colosi, Peter C.
 TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
 TITLE OF INVENTION: BY TARGET
 TITLE OF INVENTION: CELLS
 FILE REFERENCE: AVIGEN-03743
 CURRENT APPLICATION NUMBER: US/09/364, 862
 CURRENT FILING DATE: 1999-07-30
 EARLIER APPLICATION NUMBER: 60/125, 974
 EARLIER FILING DATE: 1999-03-24
 EARLIER APPLICATION NUMBER: 60/104, 994
 EARLIER FILING DATE: 1998-10-20
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 13
 LENGTH: 11933
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-09-364-862-13

Query Match 81.6%; Score 252; DB 4; Length 11933;
 Best Local Similarity 88.6%; Pred. No. 6, 6e-68;
 Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 atgcaggataaaagatgaaaaaatgttatctcgccgttggcaatgttattaca 60
 Db 9295 atcggggataaacacctgaaaaaatgttactcgctactgtcgccgttggcaatgttattaca 9354
 Qy 61 ggatgttctcaacaaacgttctcggtggaaacaaacgcacagcggatcacaaaggaa 120
 Db 9355 ggatgttctcaacaaacgttctcggtggcaatgttggcaacaaacggcggatcacaaaggaa 9414
 Qy 121 accatccctcatccatcttcgttccggaaatggcaaggaaactgttggatcgcc 180
 Db 9415 accatccatccatccatcttcgttccggaaatggcaaggaaactgttggatcgcc 9474
 Qy 181 aatgttgggggtggagaaatgttggtaaacacggaaactccggaaacattcgtaat 240
 Db 9475 aatgttgggggtggagaaatgttggtaaacacggaaacattcgtaat 9534
 RESULT 14
 US-08-43-637B-1
 Sequence 1, Application US/08743637B
 Patent No. 5994066

GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: PICARD, Francois J.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROU, Paul H.
 TIME OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
 TIME OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
 TIME OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: QUARLES & BRADY
 STREET: 411 EAST WISCONSIN AVENUE
 CITY: MILWAUKEE
 STATE: WISCONSIN

RESULT 13
 US-09-002-361-4
 Sequence 4, Application US/09002361
 Patient No. 6329516

GENERAL INFORMATION:
 APPLICANT: Halling, Blaik
 TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
 TITLE OF INVENTION: Channels

COUNTRY: USA
ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/743,637B

FILING DATE: 04-NOV-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/526,840

FILING DATE: 11-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433

SEQUENCE/DOCKET NUMBER: 850586.90012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 277-5000

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1817 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecalis

US-08-743-637B-1

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/526,840B

FILING DATE: 11-SEP-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/304,732

FILING DATE: 12-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433

SEQUENCE/DOCKET NUMBER: 850586.90012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 277-5000

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1817 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecalis

US-08-526-840B-1

Query Match 10.9%; Score 33 6; DB 2; Length 1817;

Best Local Similarity 51.3%; Pred. No. 0.34; Mismatches 78; Conservative 0; Indels 0; Gaps 0;

Matches 78;

Query 127 actcatctttctcgatcgaaatggacaaactgtgtatcgccaaat 186

Db 1211 ACCATATGCTCCCTTGTAGATGAGTGTAGTGTAGTCAGAATGACATGAGTGTAGGAACT 1270

Query 187 tggcgcgatcgaaaatgtgtatcgaaacaaatcgaaactcgcaacatcgtaatgtatggatg 246

Db 1271 ACAGCCGGTTAGATATTAGGACAACTCAGGGCCCTGAATGAACTCTATCTGATTTG 1330

Query 247 ctgggtttatccatgtggcactataatcc 278

Db 1331 ATGGTTATATTATTCGGTGCTATATCC 1362

Search completed: July 23, 2002, 13:45:10
Job time: 511 sec

RESULT 15

US-08-526-840B-1

Sequence 1, Application US/08526840B

Patent No. 601564

GENERAL INFORMATION:

APPLICANT: OUELLIETTE, Marc G.

APPLICANT: BERGERON, Michel G.

APPLICANT: ROY, Paul H.

APPLICANT: OUELLIETTE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND

TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY

TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES

TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...

NUMBER OF SEQUENCES: 177

CORRESPONDENCE ADDRESS:

ADDRESSEE: QUARLES & BRADY

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: USA

ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

Wed Jul 24 10:09:06 2002

us-09-738-599-22.rni

Gencore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:

July 23, 2002, 13:51:26 : Search time 365.82 seconds
(without alignments)
1450.239 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 309

Sequence: 1. atgcggataataaggatgaa.....ggtatattgtctacaaatag 309

Ring table: IDENTITY_NUC
Gapext 1.0

Searched: 1736436 seqs, 85845721 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_GenSeq_032802.*

1: /SIN5/gcdata/geneseq/geneseq -emb1/NA1980.DAT:*

2: /SIN5/gcdata/geneseq/geneseq -emb1/NA1981.DAT:*

3: /SIN5/gcdata/geneseq/geneseq -emb1/NA1982.DAT:*

4: /SIN5/gcdata/geneseq/geneseq -emb1/NA1983.DAT:*

5: /SIN5/gcdata/geneseq/geneseq -emb1/NA1984.DAT:*

6: /SIN5/gcdata/geneseq/geneseq -emb1/NA1985.DAT:*

7: /SIN5/gcdata/geneseq/geneseq -emb1/NA1986.DAT:*

8: /SIN5/gcdata/geneseq/geneseq -emb1/NA1987.DAT:*

9: /SIN5/gcdata/geneseq/geneseq -emb1/NA1988.DAT:*

10: /SIN5/gcdata/geneseq/geneseq -emb1/NA1989.DAT:*

11: /SIN5/gcdata/geneseq/geneseq -emb1/NA1990.DAT:*

12: /SIN5/gcdata/geneseq/geneseq -emb1/NA1991.DAT:*

13: /SIN5/gcdata/geneseq/geneseq -emb1/NA1992.DAT:*

14: /SIN5/gcdata/geneseq/geneseq -emb1/NA1993.DAT:*

15: /SIN5/gcdata/geneseq/geneseq -emb1/NA1994.DAT:*

16: /SIN5/gcdata/geneseq/geneseq -emb1/NA1995.DAT:*

17: /SIN5/gcdata/geneseq/geneseq -emb1/NA1996.DAT:*

18: /SIN5/gcdata/geneseq/geneseq -emb1/NA1997.DAT:*

19: /SIN5/gcdata/geneseq/geneseq -emb1/NA1998.DAT:*

20: /SIN5/gcdata/geneseq/geneseq -emb1/NA1999.DAT:*

21: /SIN5/gcdata/geneseq/geneseq -emb1/NA2000.DAT:*

22: /SIN5/gcdata/geneseq/geneseq -emb1/NA2001.DAT:*

23: /SIN5/gcdata/geneseq/geneseq -emb1/NA2002.DAT:*

24: /SIN5/gcdata/geneseq/geneseq -emb1/NA2003.DAT:*

RESULT 1
ID AAA73698 standard; DNA; 309 BP.
ID AAA73698 standard; DNA; 309 BP.
ID AAA73698; XX
AC
XX DT 07-DEC-2000 (first entry)
DE Avian Escherichia coli iss cDNA.
XX KW Iss: avian; outer membrane protein; OMP; vaccine; antibacterial;
KW avian colibacillosis; septicemic; pGEX-6P-3; ss.
XX OS Escherichia coli.
XX FN US607128-A.
XX FT 11-JUL-2000.
XX FT 12-FEB-1998; 98US-0023221.
XX PR 12-FEB-1998; 98US-0023221.
XX PA (NDSU-) NDSU RES FOUND.
XX PI Nolan LK, Horne SM;
XX

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	309	100.0	309 21 AAA73698	Avian Escherichia
2	309	100.0	309 22 AAF58100	Avian E. coli isola
3	309	100.0	378 21 AAF73697	E. coli iss gene in
4	309	100.0	378 22 AAF58100	Avian E. coli isola
5	309	100.0	760 21 AAF73691	Avian Escherichia
6	309	100.0	760 22 AAF58184	Avian E. coli isola
7	273.2	88.4	309 21 AAF73694	ISS CDNA from a se
8	273.2	88.4	309 22 AAF58787	Human- E. coli isola
9	252	81.6	309 21 AAF58788	Lamida Bov gen.
252	81.6	11933 22 AAF58788	Phage lambda bor g	
252	81.6	11933 22 AAD00121	Recombinant adeno	
252	81.6	11933 22 AAD08612	Human factor VIII	
141.6	45.8	180 22 ABA88818	Escherichia coli p	
39	12.6	1023 23 AAS3939	Candida albicans p	
36.2	11.7	1685 21 AAB26702	Streptococcus pyog	
36	11.7	3783 22 AAX64094	Nucleic acid seque	
35.2	11.4	4951 20 AAX13198	Arabidopsis thalia	
34.2	11.1	1519 20 AAV64373	Enterococcus faec	
33.6	10.9	1817 17 AAV28545	E. faecalis detect	
33.6	10.9	1817 22 ABA76825	Enterococcus faeca	
33.6	10.9	5756 23 ABL12582	Drosophila melanog	
33	10.7	1263 21 AAC3008	Nicotiana alata ar	
33	10.7	1698 21 AAC36256	Glyceraldehyde 3	
33	10.7	1698 21 AAC36256	Enterococcus faec	
32.8	10.6	4380 10 AAN71839	Enterococcus faec	
32.4	10.6	4381 12 AAQ0519	Pasteurella multoc	
32.4	10.6	10461 23 ABL18718	Drosophila melanog	
32.2	10.4	408 21 AAZ80085	Staphylococcus aur	
32.2	10.4	1690 16 ARO2324	Enterococcus faec	
32.2	10.4	1690 16 ARO2324	Enterococcus faec	
32.2	10.4	2364 22 AAF77837	Enterococcus faec	
32.2	10.4	4963 22 AAF77841	Fragment of Clostr	
32	10.4	344 21 AAR21119	Human secreted pro	
32	10.4	7334 24 ABL4125	Human immune syste	
31.8	10.3	1470 22 AAH53837	S. epidermidis ope	
31.8	10.3	1470 22 AAH53892	S. epidermidis ope	
31.8	10.3	1470 22 AAH53892	Human immune/haeme	
31.8	10.3	1747 22 AAH56652	S. epidermidis gen	
31.8	10.3	2754 22 AAH56652	S. epidermidis gen	
31.8	10.3	3233 22 AAH56222	S. epidermidis gen	
31.8	10.3	3249 22 AAH52558	S. epidermidis gen	
31.8	10.3	3511 22 AAH45666	Drosophila melanog	
31.8	10.3	6034 23 ABL12986		

ALIGNMENTS

RESULT
AAF58784

Wed Jul 24 10:09:06 2002

us-09-738-599-22.rng

GenCore version 4.5
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OM nucleic - nucleic search, using sw model.

Run on: July 23, 2002, 13:43:18 ; Search time 1949.42 Seconds.

(without alignments)
 3317.038 Million cell updates/sec

Title: US-09-738-599-22

Perfect score: 309

Sequence: 1 atgcaggataatagatgaa.....gggtatattgtcacatag 309.

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pt:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_v1:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_v1:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
------------	-------	--------------	-------	-------------

Query	Match Length	DB ID	Description
BASE COUNT	101	a	/organism="Unknown"
ORIGIN	60	c	64
		g	84
		t	

Wed Jul 24 10:03:03 2002

Search completed: July 23, 2002, 13:43:20
Job time: 7471 sec

Db	7255	AAATTGTCGGCGCAGAAATGTTAACAGAACCCAGCAACATCGTAAAT	7196
Oy	241	ggatgtcggtttatccacttttgcatactataccgtggaaacctggaaactcagaaacatcgtaat	300
Db	7195	GGATGCTCGGTTTATACCTTACGCATTATACGCCGTTGAGGCGCTGATTCG	7136
Oy	301	tcacata 308	
Db	7135	TCACATA 7128	
RESULT	15		
XXU02427/C	XXU02427		
LOCUS		9205 bp	DNA
DEFINITION		linear	SYN 29-JAN-199
VERSION	U02427		
KEYWORDS		Cloning vector lambda EMBL3 SP6/T7.	
SOURCE		Cloning vector lambda EMBL3 SP6/T7	
ORGANISM		artificial sequence; vectors.	
REFERENCE	1	(bases 1 to 9205)	
AUTHORS	Kitts, P.A.		
TITLE	CLONTECH Vectors On Disc version 1.3		
JOURNAL	Unpublished		
REFERENCE	2	(bases 1 to 9205)	
AUTHORS	Kitts, P.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.		
COMMENT	1020 East Meadow Circle, Palo Alto, CA 94303, USA		
	This sequence has been compiled from information in the sequence		
	databases, published literature and other sources. If you suspect		
	there is an error in this sequence, please contact CLONTECH's		
	Technical Service Department at (415) 424-8222 or (800) 662-2566,		
	extension 3 or E-mail TSCH@CLONTECH.COM.		
FEATURES		Location/Qualifiers	
source		/organism="Cloning vector lambda EMBL3 SP6/T7"	
BASE COUNT	2546 a 2002 c 2253 g 2404 t		
ORIGIN			
Query Match	81.6%	Score 252; DB 12; Length 9205;	
Best Local Similarity	88.6%	Pred. NO. 6-48-54;	
Matches	273;	Pred. NO. 6-48-54;	
Conservative	0;	Mismatches 35;	
		Indels 0;	
		Gaps 0;	
Oy	1	atggagataataatggaaaaatgttattttcgccgtctggcaatgtttttatata 60	
Db	7470	ATCGGGATACACCATGAAAMATGCTCTCGCTACCGCTGCCGCTATAC 7411	
Jy	61	ggatgtcggtttatccacttttgcatactataccgtggaaacctggaaactcagaaacatcgtaat 120	
Db	7410	GGATGCTCGACAGAGTGTACTGTCAACACAAACCGCGCAGCATGACCAAGGAA 7351	
Oy	121	accatcatcatatcttcgttccggaaatggcaagaaatgttgcgtggacc 180	
Db	7350	ACCATCACCTCATTTCTCGTGTGTTGGAGTTGGCGCAGAGAACATGATGAGCC 7291	
Oy	181	aaatgttgccgttcagaaaatgttgcataactttgcatactataccgtggaaactcagaaacatcgtaat 240	
Db	7290	AAATTGTCGGCGCAGAAATGTTAACAGAACCCAGAAACATCGTAAT 7231	
Oy	241	ggatgtcggtttatccactttgcatactataccgtggaaacctggaaactcagaaacatcgtaat 300	
Db	7230	GGATGCTCGGTTTATACCTTACGCATTATACCTCCGCTGGAAAGCGCGTGTATTCG 7171	
	301	tcacata 308	
		7170	TCACATA 7163

002
us-09-738-599-22.rge

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GenCore version 4.5
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ON nucleic - nucleic search, using sw model1
Run on: July 23, 2002, 11:04:54 ; Search time 2538.62 Seconds
(without alignments)

2009.694 Million cell updates/sec
US-09-738-599-21

Title: Perfect score: 378
Sequence: 1 ctggaggctctgtccaggg.....ggagctcatctgcgaaattcc 378

Scoring table: IDENTITY_NUC
GPop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_eatba:*

2: em_eathum:*

3: em_eatin:*

4: em_eatmu:*

5: em_eatov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_gss:*

13: em_gss_hum:*

14: em_gss_inv:*

15: em_gss_pin:*

16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	1	ALIGNMENTS
AW619529/C	AW619529	
DEFINITION	7594 MARC PBE SUS SCROFA 332 bp mRNA sequence.	
ACCESSION	AW619529	
VERSION	AW619529.1	
KEYWORDS	EST:	
SOURCE	PIG.	
ORGANISM	Sus scrofa	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
REFERENCE	1 (bases 1 to 332)	
AUTHORS	Smith, T.P.L., Fahrenkrug, S.C., Rohrer, G.A., Simmen, F.A., Rexroad, C.E. and Keele, J.W.	
TITLE	Mapping of expressed sequence tags from a porcine early embryonic cDNA library	
JOURNAL	Anim. Genet. 32 (2), 66-72 (2001)	
MEDLINE	21314990	
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smitht@mail.marc.usda.gov	
	Single pass sequencing. Bases called and alt-trimmed with Phred v0.9804.8. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.	
PCR PRIMERS		
FORWARD:	GGAAACAGCTATGCCATG	
BACKWARD:	GTAAGACGACGGCAGT	
Seq primer:	ATTAATACCCCTCACTAAGGG.	
FEATURES	Location/Qualifiers	
source	1. .332 /organism="Sus scrofa" /db_xref="taxon:9223" /clone_id="MARC PBE" /tissue_type="Day 12 whole embryos" /lab_host="XLOLR" /note="vector: PBUESCRIPT SK-; Site_1: ECOLI; Site_2: XHOI; Library made from pool of embryos in spherical and	

NO.	Score	Query	Match Length	DB	ID	Description
c 1	232	61.4	332	9	AW619529	AW619529 7594 MARC
c 2	187.2	49.5	731	9	AV398499	AV398499 AV398499
c 3	143.8	38.0	240	9	AW659631	AW659631 97104 MAR
c 4	139.8	37.0	785	9	A1547008	A1547008 PN2..1..13..
c 5	123.8	32.8	223	10	C22108	C22108 Miya
c 6	120.9	31.9	160	10	BG895793	BG895793 359430 MA
c 7	119	31.5	160	10	BG83172	BG83172 353618 MA
c 8	109.6	29.0	162	10	B1338974	B1338974 363710 MA
c 9	109.4	28.9	336	10	BE21841	BE21841 M2201STM
c 10	89.4	23.7	178	10	BI32815	BI32815 EST35576
c 11	65.8	17.4	802	9	A1546999	A1546999 PN2..1..12..
c 12	63.7	16.7	594	9	BE493915	BE493915 WHE1276_B
c 13	45.4	12.0	299	9	AB547917	AB547917 MB3D6V2G0
c 14	45.2	12.0	60	12	B84811	B84811 RIC11-28F7
c 15	45.2	12.0	634	12	A030897	A030897 CIRB1-EL1
c 16	42.8	11.3	532	12	AQ544521	AQ544521 CIRB1-EL1
c 17	38.8	10.3	735	12	AZ131766	AZ131766 OSJNBB011

filamentous stages of development (7.5% and 92.5%, respectively, of each stage) as described in Choi et al., *Endocrinology* 137: 1457-67, 1996; ".

BASE COUNT 94 a 68 C 74 g 96 t
ORIGIN

Qy	203	ttatcgccaaatgtggggtcggaaatgttgtttaacacaaactcgaaa	262
Db	212	TGATGCGCCAAATTGTTGGGGCGCAGAAATGTGTTAACAGAACCCAGCAA	153
Qy	263	cattcgtaatggattctcggtttatactttggctctataactcggtgtggaaagccc	322
Db	152	CATTCGTAATGGATTCTCGGTTTATCTACTTTAGGCTTATACTCCGCTGGAGCCC	93
Oy	323	ggatatgttcacatgtgc	346
Db	92	GTCGATTCACATAATGCG	69

RESULT	2
LOCUS	AV398499
DEFINITION	AV398499 Bombyx mori ovary BmNPV infected; 2 hr after inoculation
ACCESSION	AV398499
VERSION	AV398499.1
KEYWORDS	EST
SOURCE	domestic silkworm.

RESULT	3
AW65931/c	AW659631
LOCUS	AW659631
DEFINITION	97104 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION	AW659631
VERSION	AW659631.1
KEYWORDS	EST, EST, cow
SOURCE	Bos taurus
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos
REFERENCE	1 (bases 1 to 240)
AUTHORS	Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Perletta, G., Holt, I., Karanyakheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL	Genome Res. 11 (4), 626-630 (2001)
MEDLINE	21180013
COMMENT	Contact: Smith, T.P.L.
COMMENT	rcsb.pdb is not Animal Research Center

REFERENCE	1; Bombyxoidae; Bombycidae; Bombyx.
AUTHORS	(bases 1 to 731)
TITLE	Mita, K., Morimoto M., Shimada, T., Okano, K. and Maeda, S.
JOURNAL	Bombyx mori cDNA
COMMENT	Unpublished (2000)
Contact:	Mita K
Genome Research Group	
National Institute of Radiological Sciences	
Anagawa, 4-9-1, Inage, Chiba 263-8555, Japan	
Email:	knitadnirs.go.jp
method:	uni-directional, sequence direction:sequenced from T3 primer
(5' -> 3')	
Project:	'Silkworm Genome Program in MAFF, and Research for the Future Program in JSPS', see 'SilkBase' at http://www.ab.a.u-tokyo.ac.jp/silkbase/ , for whole ESTdb.

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	location/Qualifiers
1. .731	
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/clone="NV021882"	
/clone_1=" <i>Bombyx mori</i> ovary BmNPV infected; 2 hr after inoculation"	
/tissue_type="ovary"	
/cell_type="Bm cultured cell"	
/dev_stage="BmNPV infected; 2 hr after inoculation"	
194 a 171: C 164 g 202 t	BASE COUNT

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Query Match: 38.0%; Score: 143.8; DB: 9; Length: 240;
 Best Local Similarity: 90.1%; Pred. No.: 5.6e-30;

SOURCE pg. ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suis; Suidae; Sus.
REFERENCE 1 (bases 1 to 160)
AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Gross, W.M., Bennett, G.A., Laegreid, W.W., and Keele, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4365
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.98094.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAAACGCTATGACCAT
BACKWARD: GTTTTCGAGTCAGCAGC
Plate: 123 row: L column: 23
Seq primer: ATTAGGTGACACTATAG.
FEATURES source
location/Qualifiers 1. 160
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 46 a 37 c 31 g 46 t
ORIGIN
Query Match 31.9%; Score 120.6; DB 10; Length 160;
Best Local Similarity 93.3%; Pred. No. 1 7e-23; Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Matches 126; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Oy 212 ccaaaattgtggcggtggaaatgtgttaaacagaactcgccggatcgtaa 271
Db 160 CCAAAATTGTGGCGGCGAGAAAGTTGTTAACAGAAACCCAGAACATCGTA 101
Oy 272 atggatgtcgccgtttatcacctttggcatctatccctggaaaggccggatatt 331
Db 100 ATGGATGTCTGGTTTATACCTTAGGATTATACCCGGAGGCCGGTATT 41
Oy 332 gtcacaaatgttc 346
Db 40 GCTCACATAATTGTC 26
RESULT 7
LOCUS BG835172/c
DEFINITION 160 bp mRNA linear EST 25-MAY-2001
ACCESSION BG835172
VERSION BI338974.1
KEYWORDS EST.
SOURCE pg.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suis; Suidae; Sus.
REFERENCE 1 (bases 1 to 160)
AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Gross, W.M., Bennett, G.A., Laegreid, W.W., and Keele, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.98094.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
REFERENCE 1 (bases 1 to 160)
AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Gross, W.M., Bennett, G.A., Laegreid, W.W., and Keele, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.98094.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 634)
 REFERENCE
 AUTHORS Adams, M.D., Rounsaville, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
 Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M., and
 Venter, J.C.
 TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
 Map Building (1998)
 JOURNAL Unpublished (1998)
 COMMENT Other GSBS: CITB1-E1-2522C23.TF
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genetics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbt@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
http://www.tigr.org/tgb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.
 FEATURES Location/Qualifiers
 source 1 .. 634.
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2522C23"
 /clone_id="CITB1-E1"
 /sex="male"
 /cell_type="sperm"
 /note="vector: PBlabBAC1; site_1: EcoRI; site_2: EcoRI;
 BASE COUNT 274 a 123 c 89 g 148 t
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 Best Local Similarity 48.8%; Pred. No. 0.037; 122; Conservatve 0; Mismatches 128; Indels 0; Gaps 0;
 Matches 122; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
 QY 41 ataaataatagatggaaaaatgttattttcgccgtctggaaatgtttatccaggatgt 100
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 Db 309 ATTGAACTACAGACAGAAGCTACTTGCTACTGCTACTGCTACTGAGTG 368
 QY 101 ctccacaaacgtttactgttggaaacaaacccggacggacgttaacccaaaggaaaccatca 160
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 Db 369 CTAGCCAGAACATCAGGTAAGTAAATCAAGGCGTCAAACAAAGAAGTCAAA 428
 QY 161 ctccatcatcttcgttttggggatggacaaactgttgtatggcggcaattt 220
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 Db 429 TATCTCTCATCATGGATTATAAATCTATACTAGAGAACCTGAGACACCCAAAGA 488
 QY 221 ggggggtggaaaaatgtgttaacggaaactcggaaatccggaaatggatgc 280
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 Db 489 CTCCGGTGTACTGATGATGATGTCAGTAAATGTCAGGATACAAATAGTGCACAAATAG 548
 QY 281 tcgttttat 290
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 Db 549 TAGCATTT 558

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 Job time: 7536 sec

OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0502017.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX DR P-PSDB; ABC9752.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess PT biodiversity -
 XX PS Claim 1; SEQ ID No 29743; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS6197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.
 Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX SQ Sequence 1023 BP; 272 A; 267 C; 267 G; 217 T; 0 other;
 XX Query Match 10.3%; Score 39; DB 23; Length 1023;
 XX Best Local Similarity 81.8%; Pred. No. 0.08%; Mismatches 10; Indels 0; Gaps 0;
 XX Matches 45; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Qy 62 tattttctggcgttggcaatgttattacaggatgtctacaacagtta 116
 Db 1022 TACTCGCTACTGGCTGGCTTATCAGGATGCTCACAGACATTAC 968
 RESULT 15
 XX ID AAS26702 standard; cDNA; 1685 BP.
 XX AC AAS26702;
 XX DT 23-JUN-2000 (first entry)
 XX DE Candida albicans polynucleotide sequence #40.
 XX KW Candida albicans infection; growth; survival; medicament; AIDS;
 KW vulvovaginitis; immunocompromised patient; treat; ss.
 XX

OS Candida albicans.
 XX PN EP982401-K2.
 XX PD 01-MAR-2000.
 XX PF 23-DEC-1998; 98EP-0310694.
 XX PR 14-AUG-1998; 98GB-0011796.
 XX PA (JANCO) JANSSEN PHARM NV.
 XX PI Contreras RH, Nelissen B, De Backer MD, Luyten WHM, Viaene JE;
 XX PI Loghe MG;
 XX DR WPI; 2000-258614/23.
 XX PT Essential polypeptides isolated from Candida albicans, useful in the treatment of diseases caused by C.albicans, especially in immunocompromised subjects, e.g., AIDS patients -
 XX PS Claim 1; Page 78; 133pp; English.
 XX CC This sequence represents a polynucleotide sequence encoding a polypeptide that is critical for the survival and growth of Candida albicans. The CC C. albicans nucleic acid molecules of the invention may be used as probes CC and primers for detecting homologous nucleic acid molecule sequences. CC The polypeptides and nucleic acid molecules and compounds identified as CC selectively modulating the expression of the polypeptides, may be used as CC medicaments or for the preparation of a medicament to treat C.albicans CC associated diseases, especially in AIDS patients and to treat CC vulvovaginitis in otherwise healthy females. The use of the polypeptides CC and polynucleotide sequences to treat C.albicans associated diseases has CC fewer side effects and less toxicity than previously used methods such as CC the use of amphotericin. This method is therefore especially suitable for CC immunocompromised patients, such as AIDS patients.
 XX SQ Sequence 1685 BP; 650 A; 281 C; 250 G; 504 T; 0 other;
 XX Query Match 9.9.6%; Score 36.2; DB 21; Length 1685;
 XX Best Local Similarity 59.0%; Pred. No. 0.81; 43; Indels 0; Gaps 0;
 XX Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 142 acaccaaggaaaccatcactcatcatttcgttccggaaatggcaaggaaact 201
 Db 1334 acaccacccggaaaccacccatataatcatacgttgcgtatggaaaggatgaaatt 1393
 Qy 202 gttgtatgcggccataatgtggggcgaaatgtgttata 246
 Db 1394 agtgtatgtatgtttatctgtatggaaaggatgaaatgttattggaa 1438
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 Job time: 5377 sec

Wed Jul 24 10:09:00 2002

us-09-738-599-21.rng

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GenCore version 4.5

On nucleic - nucleic search, using sw model

run on: July 23, 2002, 12:19:59 : Search time 99.46 Seconds
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Scoring table: IDENTITY.NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /rcgn2.6/ptodata/2/ina/6A.COMB.seq:*

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5: /rcgn2.6/ptodata/2/ina/PCTRUS.COMB.seq:*

6: /rcgn2.6/ptodata/2/ina/Backfileseq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	339.8	89.9	760	4	US-09-202-352A-1
5	309	81.7	309	4	US-09-033-221A-22
6	309	81.7	309	3	US-09-202-352A-22
7	273.2	72.3	309	3	US-09-033-221A-5
8	273.2	72.3	309	4	US-09-202-352A-5
9	256.4	67.8	11933	4	US-09-470-618-13
10	256.4	67.8	11933	4	US-09-304-862-13
11	252	66.7	309	4	US-09-202-352A-6
12	252	66.7	309	4	US-09-202-352A-6
13	34.2	9.0	1519	4	US-09-032-361-4
14	33.6	8.9	1817	2	US-08-733-637B-1
15	33.6	8.9	1817	3	US-08-536-840B-1
16	32.8	8.7	4380	1	US-07-542-945-1
17	32.8	8.7	4380	3	US-08-433-141-1
18	32.8	8.7	4380	3	US-08-233-314-1
19	32.4	8.6	1925	2	US-08-533-438A-1
20	32.2	8.5	408	1	US-09-338-111-169
21	32.2	8.5	1690	1	US-08-276-452A-24
22	32.2	8.5	1690	2	US-08-738-744-24
23	31.2	8.3	90050	4	US-09-245-041-5
24	30.6	8.1	1504	2	US-08-878-989-10
25	30.6	8.1	1504	4	US-09-272-796-10
26	30.6	8.1	1576	2	US-09-177-382-1
27	30.2	8.0	2089	1	US-08-552-142A-1

RESULT 1
US-09-023-221A-21

Sequence 21, Application US/09023221A
Patent No. 6087128

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLY M.
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: U.S.A.
ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,221A
FILING DATE: 12-FEB-1998
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010101
TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1226
TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-09-023-221A-21

Query Match 100.0%; Score 378; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 3 2e-112;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctggaaatcgatcgatccggggccctgggatccatcaggataataggatggaaatgt 60
Db 1 CTGGAAATCGATCGATCCGGGGCCCTGGGATCCATCAGGATAATAGGATGGAAATGT 60

QY 61 ttatcttcgtggcgtctggcaatgttattacagatgtgcacaacaaacgtttactgtt 120
 DB 61 TTTTTCGCGCTCTGGCAATGCTTACAGGTGCTCACAACTTACTGTT 120
 QY 121 gggaaacaaacccggacggcgttacacaaaaggaaaccatctacatcttttcgttcg 180
 DB 121 GAAACAAACCCGGACAGCAGTACACCAAGGAACCATCCTCATTCGCG 180
 QY 181 gggatggcagaagaactgttgcggcggaaattingggcgatggaaatgtt 240
 DB 181 GGAATGGACAGAGAAACTGTGTCAGCCAAATTGGGG 240
 QY 241 gttaaacacagaactcggcaacatcgtaatggatgtcggtttatcaactttggc 300
 DB 241 GTTAACAGAGAAACTCGCAACATCGTAAATGGATGCGGTTTACACTTGGC 300
 QY 301 atctatactccgtggaaagccgggtatattgttccaaataggatggccatcgatggg 360
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 QY 361 agtcatctggggatcc 378
 DB 361 AGCTCACTCGGAATCC 378

RESULT 2
 US-09-282-352A-21
 ; Sequence 21, Application US/09282352A
 ; Patent No. 6187321

GENERAL INFORMATION:
 APPLICANT: NOLAN, LISA K.
 APPLICANT: HORNE, SHELLEY M.
 TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
 NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
 ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
 STREET: 119 NORTH FOURTH STREET, SUITE 203
 CITY: MINNEAPOLIS
 STATE: MN
 COUNTRY: U.S. A.
 ZIP: 55401

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/282,352A
 FILING DATE: 31-MAR-1999

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/023,221
 FILING DATE: 12-FEB-1998

ATTORNEY/AGENT INFORMATION:
 NAME: SANDBERG MS., VICTORIA A.
 REGISTRATION NUMBER: 41,287
 REFERENCE/DOCKET NUMBER: 255.00010102

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 305-1226
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 378 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-282-352A-21

RESULT 3
 US-09-023-221A-1
 ; Sequence 1, Application US/09023221A
 ; Patent No. 6087128

GENERAL INFORMATION:
 APPLICANT: NOLAN, LISA K.
 APPLICANT: HORNE, SHELLEY M.
 TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
 NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
 ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
 STREET: 119 NORTH FOURTH STREET, SUITE 203
 CITY: MINNEAPOLIS
 STATE: MN
 COUNTRY: U.S. A.
 ZIP: 55401

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,221A
 FILING DATE: 12-FEB-1998
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: SANDBERG MS., VICTORIA A.
 REGISTRATION NUMBER: 41,287
 REFERENCE/DOCKET NUMBER: 255.00010101
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 305-1226
 TELFAX: (612) 305-1228
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 760 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-023-221A-1

Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctggaaatgtcggtccaggggccctggatccatcgaggataatggataaaaatgt 60
 DB 1 CTGGAATGTCGCTTCAGGGCCCGGGGATGCGATGCGGAAATAGCAAAATG 60
 QY 61 ttatcttcgtggcgtctggcaatgttgcggatcttcacatgttgcgttt 120
 DB 61 TTTTTCGCGCTCTGGCAATGCTTACAGGTGCTCACAACTTACTGTT 120
 QY 121 gggaaacaaacccggacggcgttacacaaaaggaaaccatctacatcttttcgttcg 180
 DB 121 GAAACAAACCCGGACAGCAGTACACCAAGGAACCATCCTCATTCGCG 180
 QY 181 gggatggcagaagaactgttgcggcggaaattingggcgatggaaatgtt 240
 DB 181 GGAATGGACAGAGAACTGTGTCAGCCAAATTGGGG 240
 QY 241 gttaaacacagaactcggcaacatcgtaatggatgtcggtttatcaactttggc 300
 DB 241 GTTAACAGAGAACTCGCAACATCGTAAATGGATGCGGTTTACACTTGGC 300
 QY 301 atctatactccgtggaaagccgggtatattgttccaaataggatggccatcgatggg 360
 DB 301 ATCTATACCTCCGCTGGAGGCCGGTATATGCTACAAATAGTTGGCGGTCG 360
 QY 361 agtcatctggggatcc 378
 DB 361 AGCTCACTCGGAATCC 378

Query Match 100.0%; Score 378; DB 4; Length 378;
 Best Local Similarity 100.0%; Pred. No. 3.2e-112;

Query Match 81.7%; Score 309; DB 3; Length 309;
 Best Local Similarity 100.0%; Pred. No. 4.2e-90; Mismatches 0; Indels 0; Gaps 0;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 atgcadgatataaaggtaaaaaatgttattttccgccttgcacatgttttaca 93
 DB 1 ATGCAGGATAAAAGTAAAGGAAAGAAATGTTATTTCTGGCAATGCTTAACTA 60

QY 94 ggatggctcaacaacgtttactgttggaaacaacccggacacggaa 153
 DB 61 GGATGGCTCACAAAGTGTCTGGCAAGGAACTGTTGACGCC 180

QY 214 aaatrttgccgggtccagaaatgtgttacatcgatccatatactccgtggaaacccggatatgc 273
 DB 181 AAATTTGTCGCGGGTCAGAAATGTTAAACAGAACTCACAACTTCAATT 240

QY 274 ggatgtctcggtttatcacttttgcatctatactccgtggaaacccggatatgc 333
 DB 241 GGATGCTCGTTATCACTTGGCATCTAATCCCTGGAAAGCCGGTATATGC 300

QY 334 tcacaatag 342
 DB 301 TCACATAG 309

RESULT 6
 US-09-282-352A-22

; Sequence 22, Application US/09282352A
 ; Patent No. 6107321
 ; GENERAL INFORMATION:
 ; APPLICANT: NOLAN, LISA K.
 ; APPLICANT: HORNE, SHELLEY M.
 ; APPLICANT: ROBINSON, MICHAEL
 ; TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MURTING, RAASCH & GEBHARDT P.A.
 ; STREET: 119 NORTH FOURTH STREET, SUITE 203
 ; CITY: MINNEAPOLIS
 ; STATE: MN
 ; COUNTRY: U. S. A.
 ; ZIP: 55401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/282,352A
 FILING DATE: 31-MAR-1999
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/023,221
 FILING DATE: 12-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: SANDBERG MS., VICTORIA A.
 REGISTRATION NUMBER: 41,287
 REFERENCE/DOCKET NUMBER: 255.00010102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 305-1226
 TELEFAX: (612) 305-1226
 TELEX: (612) 305-1228
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 base pairs
 REFERENCE/DOCKET NUMBER: 255.00010102
 TELEPHONE: (612) 305-1226
 TELEFAX: (612) 305-1228
 ATTORNEY/AGENT INFORMATION:
 NAME: SANDBERG MS., VICTORIA A.
 REGISTRATION NUMBER: 41,287
 REFERENCE/DOCKET NUMBER: 255.00010102
 TELEPHONE: (612) 305-1226
 TELEFAX: (612) 305-1228
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

Query Match 81.7%; Score 309; DB 4; Length 309;
 Best Local Similarity 100.0%; Pred. No. 4.2e-90; Mismatches 0; Indels 0; Gaps 0;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 atgcadgatataaaggtaaaaaatgttattttccgccttgcacatgttttaca 93
 DB 1 ATGCAGGATAAAAGTAAAGGAAAGAAATGTTATTTCTGGCAATGCTTAACTA 60

QY 94 ggatggctcaacaacgtttactgttggaaacaacccggacacggaa 153
 DB 61 GGATGGCTCACAAAGTGTCTGGCAAGGAACTGTTGACGCC 180

QY 214 aaatrttgccgggtccagaaatgtgttacatcgatccatatactccgtggaaacccggatatgc 273
 DB 181 AAATTTGTCGCGGGTCAGAAATGTTAAACAGAACTCACAACTTCAATT 240

QY 274 ggatgtctcggtttatcacttttgcatctatactccgtggaaacccggatatgc 333
 DB 241 GGATGCTCGTTATCACTTGGCATCTAATCCCTGGAAAGCCGGTATATGC 300

QY 334 tcacaatag 342
 DB 301 TCACATAG 309

RESULT 7
 US-09-023-221A-5
 ; Sequence 5, Application US/09023221A
 ; Patent No. 6087128
 ; GENERAL INFORMATION:
 ; APPLICANT: NOLAN, LISA K.
 ; APPLICANT: HORNE, SHELLEY M.
 ; TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MURTING, RAASCH & GEBHARDT P.A.
 ; STREET: 119 NORTH FOURTH STREET, SUITE 203
 ; CITY: MINNEAPOLIS
 ; STATE: MN
 ; COUNTRY: U. S. A.
 ; ZIP: 55401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,221A
 FILING DATE: 12-FEB-1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: SANDBERG MS., VICTORIA A.
 REGISTRATION NUMBER: 41,287
 REFERENCE/DOCKET NUMBER: 255.00010102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 305-1226
 TELEFAX: (612) 305-1228
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

US-09-023-221A-5
 US-09-282-352A-22

Sequence 6, Application US/09282352A

Patent No. 6187321

GENERAL INFORMATION:

APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

APPLICANT: ROBINSON, MICHAEL

TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEETING, RAASCH & GEBHARDT P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: U.S.A.

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/282,352A

FILING DATE: 31-MAR-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/023,221

FILING DATE: 12-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG MS, VICTORIA A.

REGISTRATION NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 255.00010102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1226

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: DNA (genomic)

US-09-282-352A-6

Query Match 66.7%; Score 252; DB 4; Length 309; Best Local Similarity 88.6%; Pred. No. 8.4e-72; Matches 273; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Query Match 9.0%; Score 34.2; DB 4; Length 1519; Best Local Similarity 67.6%; Pred. No. 0.15; Matches 48; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Db 1 ATCGGAAATACACCATGAAAAAATGCTACTGCGCTGCCCTATTAAC 60

Qy 94 gatgtgtgtcaacaacaaatgtttactgttgcggaaacaaccggaggatcaacccaaagaa 153

Db 61 GATGATGTCACAGACAGTCAGTACGACAGCAACAGGAA 120

Qy 154 accacactcatcattcttcgttccggaaatggacaagaaactgttgcgtggcc 213

Db 121 ACCATCACCCATCATCATCTGTTGGAATGGCCAGAGAAACTGTGATGCCAGCC 180

Qy 214 aaaaattgtgggggtcgagaaatgtgttaaacagaacactcagaacatcgtaat 273

Db 181 AAATTGTGGGGCGAGAAATGCTAAACAGAACCCACAAATCGTAAT 240

Qy 274 ggatgtgtcggtttatcacttttcgtcatctatactccgttgcggatattgc 333

Db 241 GGATGTCCTCGTTTATTACCTTACGCATTATACGCCGCGGCGTGTATTGC 300

Qy 334 tcacata 341

Db 301 TCACATA 308

RESULT 13

US-09-002-361-4

Sequence 4, Application US/09002361

Patent No. 6359516

GENERAL INFORMATION:

APPLICANT: Halling, Blaik

TITLE OF INVENTION: Leptoapteran GABA-Gated Chloride

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08443

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/002,361

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: BLOOM, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-520-3214

TELEFAX: 609-520-3259

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1519 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLogy: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1..1443

OTHER INFORMATION:

US-09-002-361-4

RESULT 14

US-08-743-637B-1

Sequence 1, Application US/08743637B

Patent No. 5590066

GENERAL INFORMATION:

APPLICANT: BERGERON, Michel G.

APPLICANT: PICARD, Francois J.

APPLICANT: OUELLETTE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA

TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
 TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: QUARLES & BRADY
 STREET: 411 EAST WISCONSIN AVENUE
 CITY: MILWAUKEE
 STATE: WISCONSIN
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/743,637B
 FILING DATE: 04-NOV-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/526,840
 FILING DATE: 11-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586.90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5000
 TELEFAX: (414) 277-5591
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1817 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecalis
 US-08-743-637B-1

Query Match 8.9%; Score 32.6; DB 2; Length 1817;
 Best Local Similarity 51.3%; Pred. No. 0.25; DB 2;
 Matches 78; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 160 actccatcttcgttcggaaatggatcgccaaatt 219
 DB 1211 ACTCCATCTTCGTTCGGAAATGGATCGCCAAATT 1270
 QY 220 tggcgatgcggaaatgtttaaacacagaactcgaaacatccgttaatggatg 279
 DB 1271 ACTCCATCTTCGTTCGGAAATGGATCGCCAAATT 1330
 QY 280 ctggtttatactttggcatctatacc 311
 DB 1331 ATGGTTATATTTGGGTGATCTATCC 1362

Search completed: July 23, 2002, 13:45:07
 Job time: 5108 sec

RESULT 15
 US-08-743-637B-1
 Sequence 1, Application US/08/743,637B
 Patent No. 6001564
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: ODELLERTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
 TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
 TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
 TITLE OR INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
 NUMBER OF SEQUENCES: 177
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: QUARLES & BRADY

Wed Jul 24 10:09:01 2002

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Page 9

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